IN THE CLAIMS:

Claims 1-5 (canceled).

Claim 6 (withdrawn/currently amended) A method for the identification of ~~the~~ an animal from a biological sample comprising DNA of the animal, said method comprising the steps of:

a) isolating and amplifying the DNA ~~from the biological sample to be tested using~~ with the ~~primers~~ primer pair as claimed in claim ~~1~~; 17to form amplified products,

b) sequencing the amplified products,

c) blasting the sequence resolved in step (b) against ~~mito~~ a database ~~of National Centre for Biotechnology Information (NCBI) using BLAST program~~ and determining the most likely family of the animal source of the biological sample,

d) blasting the sequence resolved in step (b) against a non-redundant (nr) database ~~nr National Centre for Biotechnology Information (NCBI) using BLAST program~~ and determining the most likely genus, species or ~~more precisely the~~ sub-species of the animal source of the biological sample,

e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

f) isolating and amplifying and sequencing the DNA sequences from the reference ~~animal~~ animals on both strands in triplicate using the primer pair ~~primers as claimed in claim 1~~.

g) aligning the sequences obtained ~~using CLUSTRAL program~~ and identifying the

variable sites amongst the animals analyzed.

h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.

Claim 7 (cancelled)

Claim 8 (withdrawn) A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ηg of template DNA, 100 µm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HC1, pH 8.3, and 50mM KC1). The amplification profiles followed should be: an initial denaturation at 95 °C for 45 s, annealing at 51 °C for 1 min, and extension at 72 °C for 2 min. The extension step at 35^{th} cycles should be held for 10 min.

Claim 9. (withdrawn) A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Claim 10 (withdrawn) A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.

Claim 11 (withdrawn) A method as claimed in claim 6 wherein the method is used to establish the identity of biological materials such as skin, horns, etc confiscated from animal poachers, if it is that of an endangered species.

Claim 12 (withdrawn) A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.

Claim 13 (withdrawn) A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.

Claim 14 (withdrawn) A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.

Claim 15 (withdrawn) A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic

scientists with human blood.

Claim 16 (withdrawn) A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECUALR KIT' and (b) "DNA CHIPS' based applications for wildlife identification in forensics.

Claim 17 (new) A universal primer pair for amplifying a fragment of cytochrome b gene of an animal species in a polymerase chain reaction (PCR) or determining the identity of the biological material of an animal of unknown origin at species and sub-species level, said primer pair essentially comprising SEQ ID NO: 1 and SEQ ID NO: 2.

Claim 18 (new) A reaction mixture comprising the primer pair of claim 1 and a fragment of a mitochondrial cytochrome b gene flanked by sequences that are highly conserved amongst a range of animal species.

Claim 19 (new) The reaction mixture as claimed in claim 18, wherein the fragment of mitochondrial cytochrome b gene is polymorphic inter-specifically but monomorphic at intra species sources.

Claim 20 (new) The reaction mixture as claimed in claim 18, wherein the fragment comprises SEQ ID NO: 211.

Claim 21 (new). The universal primer pair as claimed in claim 17, which consists essentially of SEQ ID NO: 1 AND SEQ ID NO: 2.

Claim 22 (new). The universal primer pair as claimed in claim 17, which consists of SEQ ID NO: 1 and SEQ ID NO: 2.

Claim 23 (new). An isolated primer consisting essentially of SEQ ID NO: 1.

Claim 24 (new). The primer of claim 23, which consists of SEQ ID NO: 1.

Claim 25 (new). An isolated primer consisting essentially of SEQ ID NO: 2.

Claim 26 (new). The primer of claim 25, which consists of SEQ ID NO: 2.